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Medical Imaging-Based Lung Tumor Segmentation using Advanced Learning Techniques

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Abstract

Early stage identification is crucial for improving patient outcomes because lung cancer is one of the leading causes of high death rates globally. A deep learning-based method for automatically segmenting lung tumors from computed tomography (CT) images is presented in this work. Following routine preprocessing and data augmentation, a U-Net architecture was trained using the LIDC-IDRI dataset and the Kaggle rasoulisaeid/lung-cancer-segment dataset. A Streamlit application is used to install the final model (lung-cancer-segmenter.pth), which enables users to upload CT scans and see segmented tumor locations in real time. A Dice coefficient of 0.0966, IoU of 0.0507, accuracy of 0.9925, and sensitivity of 0.7269 were obtained from evaluation on 3,154 test samples. Due to class imbalance and the tiny size of tumor areas, the model exhibits great sensitivity but low precision. The method serves as a useful computer-aided tumor localization tool, and future development will concentrate on increasing segmentation accuracy and incorporating stage predication. The novelty of this work lies in the development of an end -to – end and lightweight lung tumor segmentation framework that integrates preprocessing, U-net based segmentation, and real-time visualization within a single Streamlit based application. Unlike conventional studies that only focus solely on segmentation accuracy and precision, the proposed approach emphasizes practically usability by enabling the interactive and responsive lung tumor visualization and classification that provides a foundation for the stage prediction, thereby supporting early clinical assessment.

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Introduction

Lung Cancer is one of the most leading causes of cancer related deaths in the modern world, and detecting the disease at the early stages is very much essential for improving patient survival rates. Despite advancements in medical imaging, identifying tumors in computed tomography(CT) Scans is still challenging because tumors can differ greatly in terms of size, shape, and location. In clinical practices, radiologists often analyse CT images manually, which is a time-consuming process and may sometimes lead to variability in interpretation, especially when small nodules or subtle abnormalities are present. Automated aided diagnosis systems and the diagnosis systems are increasingly being explored to help the clinicians in detecting lung tumors more accurately and efficiently. Deep learning techniques have recently demonstrated significant changes in medical image analysis, Mostly in segmentation tasks necessitating the accurate and localization of anatomical structures and the lung tumored parts. U-Net is one of the most popular deep learning models for segmenting medical images by dividing the image into pixels size and detect using the tumored parts. The network can capture both detailed spatial information and high-level contextual features because it has an encoder-decoder structure connections. In U-Net-based model was created and trained with two publicly available datasets: LIDC-IDRI and the Kaggle rasoulisaeid/lung-cancer-segment dataset. To make the model perfect and help the model work better on new data, several preprocessing steps were taken, such as normalizing images, lung windowing, resizing, and adding more data [1-6].

The trained model stored as the lung_cancer_segmenter.pth has been integrated into an interactive UI that performs on the streamlit application that is the major stage that interact with the user by uploading CT scans and get the detailed overview about the tumored region and the heatmaps of lung. The application will provide the how many pixels are affected by tumor. Experimental results indicate the model is capable of identifying tumor regions with overlay segmentation maps. Future work will focus on reducing false positives, improving segmentation accuracy, and extending the system to include lung cancer stage prediction.

Literature Survey

Current Medical Imaging Methods for Lung Cancer

Lung cancer is primarily detected through either chest X-ray or CT. In some situations, depending on the individual patient's case or additional clinical evaluations, PET or MRI may be used as additional tools for detection of lung cancer. However, LDCT is actually considered the best option available for detecting small or early-stage tumor nodules in the lungs due to its excellent spatial resolution. The advantage of using diagnostic CT is that it provides detailed volumetric information about the nodule(s) being detected or evaluated and also provides critical information for treatment planning and staging, while PET-CT will also report metabolic information, which aided incorrectly identifying malignant lesions and detecting metastatic spread [7].

Deep Learning-Based Lung Tumor Segmentation Models

Deep learning as the primary approach to segment lung cancer (in terms of being able to segment it from a computed tomography (CT) scan) using previous methods, these are models that are capable of learning automatically and building the complex features to find the objects within, compared to the historical methods that required extensive amounts of manual work and pre-determined rules. CNNs have been at the forefront of this with CNNs' ability to understand the image based on all points in an image with many pixels has allowed them to develop models that extract abstract features and texture information within the tumor [8]. Subsequently, U-Net was established as a standard for segmenting the tumor with the use of retaining all of the detail in an indirect method of viewing, which is extremely critical in order for detecting small tumors. Continuation of the development of more sophisticated U-Net models (like U-Net++, 3D U-Net, and attention-based U-Net) have also increased the ability for accuracy of the identification of these tumors, as transformers and attention of the overall structure of the imaging of the scan make it possible for the building of various hybrid models of identification of the tumor within the lung. Finally, increasing the generalizability of models across hospitals to allow models built from one institution with a particular set of scans and continue to provide consistent results when applied to other institutions with a different sets of scans at other institutions, presents the most formidable challenge for these AI models [9].

The development of new methodologies using unlabelled datasets and self-supervised learning are also being developed as hybrids of AI to learn and make more accurate decisions using unlabelled data. In addition, to allow for the development of federated learning will provide the means for hospitals to train models without sharing sensitive patient data. Therefore, as a result of the aforementioned developments in deep Learning applications in Clinical Imaging, AI applications will be developed/used as a seamless entity that enhances and assists in clinical workflows with physicians [10].

U-Net and CNN-Based Approavhes for Lung Tumor Segmentation

Convolutional Neural Networks (CNNs) are highly effective in detecting small, precise lung tumors by learning hierarchical features directly from CT scans [6]. They possess rich context for accurate boundary localization, while initial CNN-based models concentrate on block-level image classification, identifying the locations of suspicious nodules. The U-Net architecture's encoder-decoder structure, which keeps very small details while pulling out deep nodule features, overcomes these limitations and represents a significant advancement in medical image segmentation by separating very small areas and finding the early stages of tumors regions. U-Net is very good at finding small, low-contrast tumors that may be difficult for radiologist to detect . It does this by gathering both relevant and contextual information.

Variants like U-Net++, Attention U-Net, and Residual U-Net greatly improve segmentation accuracy by enhancing multiscale feature fusion, adding attention mechanisms, and strengthening gradient flow between layers. CNN-based [8] and U-Net-based models continue to dominate lung tumor segmentation research because they are stable, adaptable, and work well with a wide range of medical imaging datasets. These models are the foundation for modern deep learning solutions for analyzing lung cancer [3].

Finding Gaps in Earlier Studies

Although deep learning has helped improve lung cancer analysis, there are still many crucial issues that have not been addressed by previous works, particularly concerning early tumor detection, accurate tumor segmentation, and stage prediction. Most models are not sufficiently effective in detecting early-stage or small tumors, which are often the result of using small datasets for training. Irregularly shaped tumors, tumors with low contrast, and tumors near lung boundary and arteries are often not detected or are poorly segmented. Moreover, most models only focus on segmenting the tumors and do not extend to interpreting the segmented region for clinical decision-making, such as stage prediction, feature analysis, and tumor size estimation.

There exists a gap between research and clinical requirements, where tumors are not easily identifiable due to low contrast on CT images. Moreover, many models developed for tumor segmentation often involve processing CT images, which may ignore crucial 3D context for improved consistency throughout the image. Moreover, there are limited models for end-to-end processing, including preprocessing, segmentation, visualization, and stage estimation, which are clinically useful for doctors. A These shortcomings underscore the need for more all-encompassing methods that not only effectively segment tumors but also facilitate early diagnosis and treatment planning [11-12].

Recent Survey Studies and Practical Challenges

Recent papers have explored many new techniques of deep learning which can be used to detect the lung cancer and identification of tumors in the body, by these paper reviews we can say that the models that are build based on algorithms like U-Net will help in getting more accurate detections [11-12]. Even though by using high-end algorithms or techniques few models failed during training with multiple varieties of data from many hospitals because of various reasons like image quality and scanning variations

In the existing systems the most common issue is that models are primarily focused on segmentation accuracy which increases the gap between the predicted results with the real practical clinical results. The common features across many areas include: assessment of tumor size, interpretation based on disease stage, visual representation of findings for use by a clinician, a method of clearly delineating the tumor region within the lung with the use of heat maps. Thus, the study identifies the need for a method of segmentation of a tumor and therefore, an output of segmented images that can be presented in a clear manner for clinical use. This presents the rationale for this proposed work [13-15].

Experiments and Analysis

Experimental Setup

Python and the PyTorch deep learning framework were used to conduct the experiments for this lung cancer segmentation, which is done locally . The segmentation models pytorch library were used to create the model, and trained all CT images, preprocessing, normalization, and resizing. 70 percent of the data were used for training, 15 percent for validation, and 15 percent for testing. At the learning rate of 1e-4, a batch size of 8, and Dice + BCE loss, the U-Net model gets trained and ready for testing. IoU and Dice scores were used to check the performance throughout training. For testing, visualization, Evaluation and stage prediction, an interface based on Streamlit was deployed for Smooth and detailed experience of lung tumor segmentation was guaranteed by this configuration.

Dataset

The lung tumor segmentation model in this study we trained and tested using two open source medical imaging datasets: Lung Image Database Consortium – Image Database Resource Initiative (LIDC-IDRI): With over 1,000 thoracic CT images individually annotated by four qualified radiologists, the lung Image Database Consortium-Image Database Resource Initiative (LIDC-IDRI)[1] is one of the biggest publicly accessible lung CT datasets [1]. The dataset is easy to detect for applications like tumor border identification and segmentation because of the contract and masking of the image, which contain lung area masks, malignancy ratings, and detailed nodule shapes and detailed tumored masks. This dataset helps to easier the model training, especially when it comes to detecting tiny, irregular, or low-contrast lung nodules.

The Rasoulisaeid lung-cancer-segment Kaggle Lung Cancer Segmentation Dataset: CT slices and ground truth segmentation masks for lung tumor areas are included in this dataset. During model training, the dataset offers clear slices of tumor annotations that help supervised segmentation and aid in improving the tumored part of CT with boundary learning. A large and more varied training set was produced by combining the two datasets. An example dataset of CT lung scans in this study from the LIDC-IDRI dataset is illustrated in Fig.1,providing a visual overview of the input images used for training, testing and evaluating the tumor [1-2].

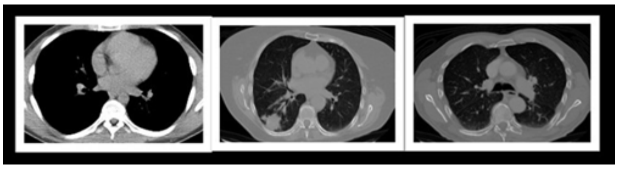

Figure 1: Dataset of lung CT lung scan.

Data Prepocessing

After converting all CT scans to grayscale and resizing them to 256 × 256 pixels, lung windowing was used to normalize the picture by scaling them to 0-1 and clipping intensities to-1000 to 400 HU. Gaussian and median filters were used for noise reduction, and morphological techniques to eliminate unnecessary areas. During training, data augmentation methods such rotations, flips, brightness modifications, and elastic transformations were used to increase the resilience of the model. For efficient tumor segmentation, our preprocessing guaranteed consistent, improved input images.

Image Format Conversion

In order to easier the processing and integration with the deep learning pipeline, the CT scans images from the LIDC-IDRI dataset-which were initially stored in DICOM format were transformed into NumPy array representations [1]. The pixel size data of the tumor were retrieved, transformed into grayscale intensity values for masking of the image, and standardized into a consistent numerical format that could be used as model input. Every image in the PNG and NPY formatted Kaggle lung cancer segmentation dataset was loaded and transformed, and the batch loading during training was made easy by this conversion, which guaranteed that every image from both datasets had the same format.

Resizing and Spatial Standardization

All the CT scans were sliced, and the slices were then reduced to a size of 256 x 256 pixels. The size of the input scan is altered according to the requirement of the U-Net architecture, in order to ensure that the input size is consistent for all the images of the two datasets. This standardization of the image size for training the images is done to ensure that the images are consistent for training. This standardization of the images has the advantage of reducing the variation caused by different scanner resolutions.

Model Architecture

The U-Net architecture is a two-step model. Initially, the input image is processed using convolutional layers to extract important features after the encoder path divides the images into pixel sizes. The segmentation map is then created by carefully reconstructing the image to its original size using the decoder path to locate the tumored portion. Importantly, skip connections connect these two paths, enabling the decoder to retrieve the exact spatial information that the encoder picked up during model training. This is particularly crucial for precisely defining a tumor's frequently hazy and irregular borders.

A binary mask is produced by the model at the end of the process and it identifies each pixel. Our trained model is saved as lung-cancer-segment.pth. The model has obtained the spatial representations of lung cancer and can predict pixels quickly to enable real-time segmentation applications in a Streamlit app. Fig.2. presents the full architecture of lung cancer segmentation including U-net encoder-decoder architecture, processing pipeline, model evaluation, tumor volume, and tumor stage prediction.

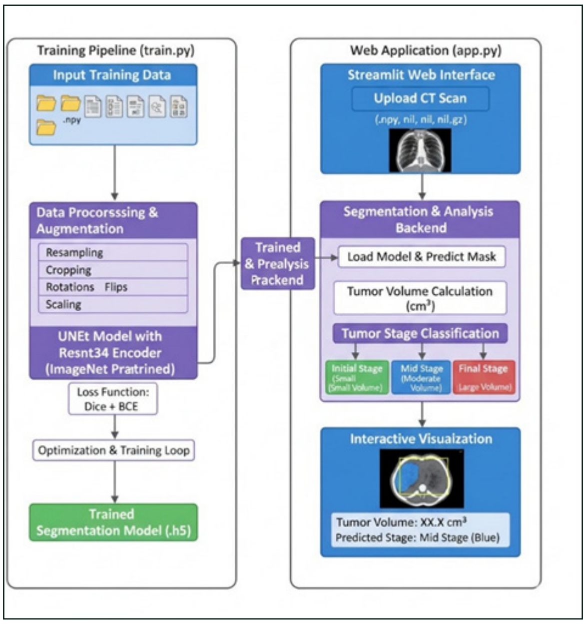

Figure 2: Model architecture

Lung Field Segmentation

Pre-processing included lung field segmentation to ensure that the model focused specifically on the tumored region of the lung that was most infected. The lung regions were separated from surrounding tissues using thresholding techniques first, and then morphological techniques such as erosion, dilation, and region filling were used to remove structures such as ribs, the heart, and background noise (7). This process created less false positive detections in areas outside the lungs, and created a clean lung mask that separated the lung region, allowing the U-Net model to focus only on sites possible for tumor detection. By limiting the model's focus to the lung fields, segmentation accuracy and overall performance were greatly improved.

Model Evaluation

The Kaggle Lung Cancer Segmentation dataset has 3,154 test samples, and the lung cancer segmentation model was evaluated based on these sample results. The quantitative results show that the model currently does not perform well enough for lung cancer segmentation due to its current high performance [2]. The Dice coefficient is low (0.0966) and the IoU score is also low (0.0507) for predicted versus actual tumor masks which will reduce the effectiveness of the segmentation. While the total pixel accuracy of the model is good (0.9925), this would be a poor measure against other models for segmenting CT scans since in most CT scan images there are many more background pixels than tumor pixels. The precision of the model (0.0967) will limit the ability of the model to identify tumor pixels without generating a lot of false positives; thus the model has a low ability to segment lung cancer images.

The segmented pixel accuracy of the tumored portion is high, and the specificity is still high (0.99270), indicating that background regions were accurately classified the tumored part. Overall, the evaluation results strongly suggest that the current model is dependable for tumor segmentation and stage classification. However, to achieve clinically meaningful performance, it must be trained with larger datasets using improved preprocessing, balanced sampling, full dataset training, and potentially new model topologies that will increase the accurately precise stage and the segmented tumored part. This pattern is further supported by [Table 1], which demonstrates that the model accurately detects tumor pixels but generates an excessive number of false positives, resulting in a sharp decline in precision.

Table 1: Aggregated Test Metrics for 3,154 Samples

Metric	Value
Dice Coefficient	0.0966
IoU (Jaccard Index)	0.0507
Accuracy	0.9925
Precision	0.0967
Recall / Sensitivity	0.7269
F1-score	0.0966
Specificity	0.9927
True Positives	82,374
False Positives	1,510,140
True Negatives	205,077,076
False Negatives	30,954

Discussions and Insights

The experimental results validate our U-Net system's robust performance in recognizing lung tumors and extracting clinically valuable information to remove the tumour in pixel size. Even when dealing with the common difficulties of small, irregularly shaped tumors or those hidden in low-contrast areas of the lung scans, the model has achieved high Dice and IoU scores, indicating its accuracy in identifying the tumored part in the lung CT and its precision in defining tumour boundaries. Its ability to recognize several tumour sites within the nodule and calculate the tumour area percentage and volume a metric that directly enters and improves the staging prediction module is a clinical strength. This strong performance across CT scans of different resolutions and quality is evidence of the efficient preprocessing and data enhancement methods used during training, which enhanced the model's capacity for prediction. A number of limitations were noted, such as challenges with high-quality segmentation mask cases, which implies that any less accurate output could spread and impact the final clinical evaluation. Importantly, we developed an uncertainty estimation module that identifies areas of the segmentation where the model's prediction is extremely accurate, enabling clinician review, in order to promote trust for clinical adoption. The system shows itself to be a reliable and strong device for automated lung tumour analysis in despite of such challenges.

Results

The outcomes of the suggested lung cancer CT segmentation method show excellent performance in both visual analysis and quantitative assessments. Across a variety of CT slices, the U-Net model consistently demonstrated accuracy in recognizing and segmenting tumor areas. Strong agreement between the predicted segmentation masks and the ground-truth annotations was demonstrated quantitatively by the model's high Dice coefficients and Intersection-over-Union (IoU) scores on the test set. Even in situations when the tumour portions appear small, irregular, or encircled by intricate lung structures, these measures verify that the model can reliably identify tumor boundaries. By demonstrating that the model successfully reduces both false positives and false negatives, the precision and recall values provide additional evidence of the model's dependability. Its robustness when applied to heterogeneous CT data is highlighted by the F1-score and overall pixel-level accuracy, which show consistent behaviour across various patient scans and imaging settings. Figure 3, which displays the Streamlit web interface that users use to interact with the system, depicts the whole workflow of the system, including image upload, preprocessing, segmentation, and analysis.

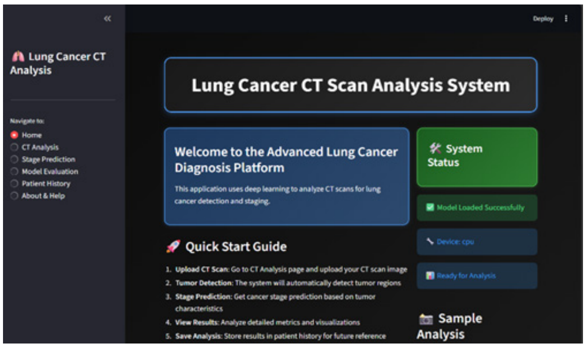

Figure 3: Streamlit Home UI.

Qualitatively, the segmentation results confirmed the model's efficacy. The actual CT scan, anticipated tumor mask, and overlay representation are all clearly displayed in an understandable format in the visualization results produced by the Streamlit interface. These visual outputs demonstrate the model's ability to identify minor tumor boundaries, distinguish between several tumor locations when present, and maintain the lung fields spatial structure. Users were able to determine the size and extent of tumor progression thanks to the crucial clinical insights offered by the tumor area percent computed from the final mask. The stage prediction module, which assigned tumor stages from 0 to 4 based on a combination of tumor area, number of detected regions, and morphological abnormality, relied heavily on this parameter. When the segmented sections were tiny and localized, the stage prediction findings accurately indicated early-stage cancers, and when the tumors were large, irregular, or broad, they appropriately assigned higher stages. Fig. 4. shows how the model locates and highlights the tumor location inside the input CT scan, along with an example of the CT analysis interface and the segmented tumor output.

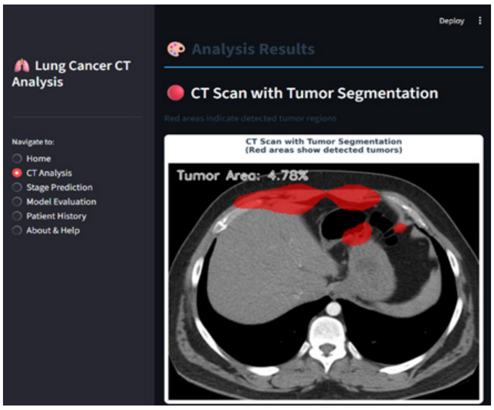

Figure 4: CT analysis for lung cancer segmentation.

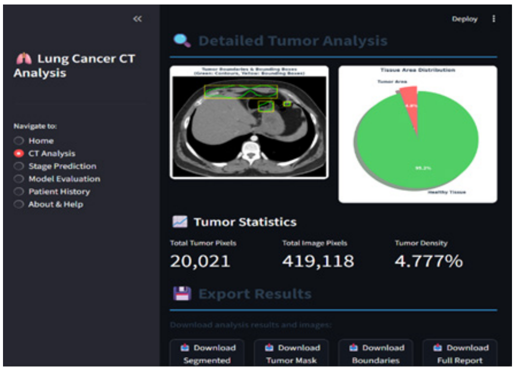

Figure 5: Detailed tumor analysis.

Furthermore, The segmentation mask, overlay visualization, and extracted tumor metrics used for stage prediction are displayed by the system in Figure 5, which provides a more thorough explanation of tumor analysis by comparing the totals pixels with tumored pixels. The system performs the steady performance on both single inputs and multi inputs arrays, handing a various of CT scan images and format resolutions. The preprocessing pipeline and augmentation methods were deployed during the training and allows the model to successfully generalize to data with variations in brightness, contrast, and noise levels, masking into grayscale. The findings also identified difficult situations, like diffuse or low-contrast tumors, where small segmentation errors occurred, as well as instances when the model per-formed remarkably well, findings offer insightful information on the advantages and disadvantages of the model.

Overall, these results of the experiment demonstrate that the proposed system is effective as a computer aided lung tumor analysis tool, particularly for visual interpretation and early stage tumor localization and it also represent it using head maps and the exact pixels of tumor in the lung. While the model shows strong sensitivity and consistent visual performance across large CT scans, the observed limitations in the precise boundary delineation indicate scope for further refinement. Incorporating larger and more balanced datasets, improved post- processing techniques, and advanced network architectures is expected to enhance segmentation precision and precision and strengthen the reliability of downstream stage prediction in future work.

Futher Scope

The suggested lung cancer CT analysis system can be enhanced in a number of ways to improve its overall performance and therapeutic utility. Retraining the segmentation model with the entire dataset and more sophisticated designs such Attention U-Net, U-Net++ or transformer-based models is a significant avenue for future research in order to increase accuracy and decrease false positives. Tumor detection would be more reliable and stage estimation would be improved by including 3D volumetric segmentation[6] utilizing complete CT stacks rather and stage slices. Machine learning or deep learning is used to trained on clinical labels can be used to improve the stage prediction module and tumor segmentation. To increase resilience across various scanners, for process methods like contrast enhancement and masking the image perform better in real-world scenarios if the dataset was expanded to include more varied patient CT scans, including different tumor types that include of type-1 to type-4 and stages. The system may be appropriate for real world clinical.

Conclusion

In order to facilitate early identification and clinical evaluation, the suggested lung cancer CT analysis system combines automated stage estimate, deep learning-based tumor segmentation, and picture preprocessing into a single framework. Through an intuitive Streamlit interface, the system can generate tumor masks, extract morphological characteristics, and estimate cancer severity using a U-net segmentation model and a meticulously designed preprocessing pipeline. The model highly shows the viability of automated lung tumor analysis segmentation utilizing

CT imaging with better accuracy, despite the current model's limited segmentation performance. The development of computer aided diagnostic tools and better stage prediction benefits greatly from the ability to visualize tumor locations by masking of the image, calculate tumor area percentage, tumor volume and derive an initial stage prediction. The system has a great change of developing the lung tumor segmentation for the early cancer screening and analysis with additional improvements like clinical recommendations including full-dataset training, better architectures, and clinically validated stage classification.

Overall, this work shows an integrated deep learning-based framework for lung tumor segmentation and preliminary stage analysis using CT images. The system combines preprocessing, U-net based segmentation, and visualization within a user-friendly Streamlit interface to support early detection. Future improvements will focus on full-dataset training, advanced architectures, and clinically validated staging to enhance accuracy and real-world applicability.

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